

DW

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PCT09

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/869,198A

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Input Set : A:\seqlistJAB1463corrected.app.txt  
Output Set: N:\CRF3\02132002\I869198A.raw

p.5

3 <110> APPLICANT: Gordon, Robert  
4 Sprengel, Jorg  
5 Yon, Jeffrey  
6 Dijkmans, Josiena  
7 Gosiewska, Anna  
8 Dhanaraj, Sridevi  
9 Xu, Jean  
11 <120> TITLE OF INVENTION: Vascular Endothelial Growth Factor-X  
13 <130> FILE REFERENCE: 51935/004  
15 <140> CURRENT APPLICATION NUMBER: US/09/869,198A  
16 <141> CURRENT FILING DATE: 2001-06-21  
18 <150> PRIOR APPLICATION NUMBER: GB 9828377.3  
19 <151> PRIOR FILING DATE: 1998-12-22  
21 <150> PRIOR APPLICATION NUMBER: US 60/124,967  
22 <151> PRIOR FILING DATE: 1999-03-18  
24 <150> PRIOR APPLICATION NUMBER: US 60/164,131  
25 <151> PRIOR FILING DATE: 1999-11-08  
27 <160> NUMBER OF SEQ ID NOS: 97  
29 <170> SOFTWARE: PatentIn Ver. 2.0  
31 <210> SEQ ID NO: 1  
32 <211> LENGTH: 323  
33 <212> TYPE: PRT  
34 <213> ORGANISM: Homo sapiens  
36 <400> SEQUENCE: 1  
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38 1 5 10 15  
40 Tyr Gly Val Gln Asp Pro Gln His Glu Arg Ile Ile Thr Val Ser Thr  
41 20 25 30  
43 Asn Gly Ser Ile His Ser Pro Arg Phe Pro His Thr Tyr Pro Arg Asn  
44 35 40 45  
46 Thr Val Leu Val Trp Arg Leu Val Ala Val Glu Glu Asn Val Trp Ile  
47 50 55 60  
49 Gln Leu Thr Phe Asp Glu Arg Phe Gly Leu Glu Asp Pro Glu Asp Asp  
50 65 70 75 80  
52 Ile Cys Lys Tyr Asp Phe Val Glu Val Glu Pro Ser Asp Gly Thr  
53 85 90 95  
55 Ile Leu Gly Arg Trp Cys Gly Ser Gly Thr Val Pro Gly Lys Gln Ile  
56 100 105 110  
58 Ser Lys Gly Asn Gln Ile Arg Ile Arg Phe Val Ser Asp Glu Tyr Phe  
59 115 120 125  
61 Pro Ser Glu Pro Gly Phe Cys Ile His Tyr Asn Ile Val Met Pro Gln  
62 130 135 140  
64 Phe Thr Glu Ala Val Ser Pro Ser Val Leu Pro Pro Ser Ala Leu Pro

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65	145	150	155	160
67	Leu	Asp	Leu	Leu
	Asn	Asn	Ala	Ile
	Asn	Ala	Ile	Thr
	Asn	Ala	Phe	Ser
	Asn	Ala	Thr	Leu
	Asn	Ala	Phe	Glu
	Asn	Ala	Asp	Asp
68		165	170	175
70	Leu	Ile	Arg	Tyr
	Ile	Arg	Tyr	Leu
	Arg	Tyr	Leu	Glu
	Tyr	Leu	Glu	Pro
			Glu	Arg
			Arg	Trp
			Trp	Gln
			Gln	Leu
			Leu	Asp
			Asp	Leu
			Leu	Glu
			Glu	Asp
71		180	185	190
73	Leu	Tyr	Arg	Pro
	Tyr	Arg	Pro	Thr
			Thr	Trp
			Trp	Gln
			Gln	Leu
			Leu	Leu
			Gly	Lys
			Lys	Ala
			Ala	Phe
			Phe	Val
			Val	Phe
74		195	200	205
76	Arg	Lys	Ser	Arg
	Lys	Ser	Arg	Val
	Ser	Arg	Val	Val
	Arg	Ser	Arg	Asp
	Ser	Arg	Val	Leu
	Asn	Asn	Leu	Asn
	Asn	Asn	Leu	Leu
	Asn	Asn	Thr	Thr
	Asn	Asn	Glu	Glu
	Asn	Asn	Val	Val
77		210	215	220
79	Leu	Tyr	Ser	Cys
	Tyr	Ser	Cys	Thr
			Thr	Pro
			Pro	Arg
			Arg	Asn
			Asn	Phe
			Phe	Ser
			Ser	Val
			Val	Ser
80		225	230	235
82	Leu	Lys	Arg	Thr
	Lys	Arg	Thr	Asp
	Arg	Thr	Asp	Thr
	Thr	Asp	Thr	Ile
			Ile	Phe
			Phe	Trp
			Trp	Pro
			Pro	Gly
			Gly	Cys
			Cys	Leu
			Leu	Leu
			Leu	Val
			Val	Lys
83		245	250	255
85	Arg	Cys	Gly	Gly
	Cys	Gly	Gly	Asn
	Gly	Asn	Cys	Ala
	Asn	Cys	Cys	Cys
	Cys	Ala	Cys	Leu
	Ala	Cys	Cys	His
	Cys	Cys	Asn	Asn
	Asn	Asn	Cys	Glu
	Asn	Asn	Cys	Cys
86		260	265	270
88	Gln	Cys	Val	Pro
	Cys	Val	Pro	Ser
	Val	Pro	Ser	Lys
	Pro	Val	Lys	Val
	Val	Thr	Lys	Thr
	Thr	Lys	Lys	Lys
	Lys	Lys	Tyr	Tyr
	Tyr	Lys	His	Glu
			Glu	Val
			Val	Leu
89		275	280	285
91	Leu	Arg	Pro	Lys
	Arg	Pro	Lys	Thr
	Pro	Lys	Thr	Gly
	Lys	Thr	Gly	Val
	Thr	Gly	Val	Arg
	Gly	Val	Arg	Gly
	Val	Arg	Gly	Leu
	Arg	Gly	Leu	His
	Gly	Leu	His	Lys
	Leu	His	Lys	Ser
	His	Lys	Ser	Leu
	Lys	Ser	Leu	Thr
	Ser	Leu	Thr	Asp
92		290	295	300
94	Val	Ala	Leu	Glu
	Ala	Leu	Glu	His
	Leu	Glu	His	His
	Glu	Glu	Cys	Asp
	His	Glu	Cys	Cys
	Glu	Cys	Asp	Cys
	Cys	Asp	Cys	Val
	Asp	Cys	Val	Cys
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104	<213>	ORGANISM:	Homo sapiens	
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	Leu	Leu	Leu	Leu
	Leu	Leu	Leu	Leu
	Leu	Leu	Leu	Thr
	Leu	Leu	Leu	Ser
	Leu	Leu	Leu	Ala
	Leu	Leu	Leu	Gly
	Leu	Leu	Leu	Gln
108	1	5	10	15
110	Arg	Gln	Gly	Thr
	Gln	Gly	Thr	Gln
	Ala	Glu	Ser	Asn
	Asn	Leu	Ser	Ser
	Asn	Leu	Ser	Lys
	Asn	Leu	Ser	Phe
	Asn	Leu	Ser	Gln
	Asn	Leu	Ser	Phe
111		20	25	30
113	Ser	Ser	Asn	Lys
	Ser	Ser	Glu	Gln
	Glu	Gln	Tyr	Gly
	Tyr	Gly	Val	Gln
	Gly	Val	Gln	Asp
	Val	Gly	Asp	Pro
	Gly	Asp	Pro	Gln
	Asp	Pro	Gln	His
	Pro	Gln	His	Glu
114		35	40	45
116	Ile	Ile	Thr	Val
	Ile	Ile	Thr	Ser
	Thr	Ile	Ser	Gly
	Ile	Ile	Gly	Ser
	Ile	Ile	Ser	Ile
	Ile	Ile	His	His
	Ile	Ile	Ser	Pro
	Ile	Ile	Pro	Arg
	Ile	Ile	Arg	Phe
117		50	55	60
119	His	Thr	Tyr	Pro
	Thr	Tyr	Pro	Arg
	Pro	Arg	Asn	Thr
	Arg	Asn	Thr	Val
	Asn	Thr	Val	Leu
	Thr	Val	Leu	Trp
	Val	Leu	Trp	Arg
	Leu	Trp	Arg	Leu
	Trp	Arg	Leu	Val
120	65	70	75	80
122	Glu	Glu	Asn	Val
	Glu	Glu	Asn	Val
	Asn	Val	Trp	Ile
	Asn	Val	Ile	Gln
	Asn	Val	Gln	Leu
	Asn	Val	Leu	Thr
	Asn	Val	Leu	Phe
	Asn	Val	Leu	Gly
	Asn	Val	Leu	Glu
123		85	90	95
125	Glu	Asp	Pro	Glu
	Asp	Pro	Glu	Asp
	Asp	Pro	Glu	Asp
	Asp	Pro	Glu	Ile
	Asp	Pro	Glu	Cys
	Asp	Pro	Glu	Lys
	Asp	Pro	Glu	Tyr
	Asp	Pro	Glu	Asp
	Asp	Pro	Glu	Phe
	Asp	Pro	Glu	Val
	Asp	Pro	Glu	Glu
126		100	105	110
128	Glu	Pro	Ser	Asp
	Pro	Ser	Asp	Gly
	Ser	Asp	Gly	Thr
	Asp	Gly	Thr	Ile
	Gly	Thr	Ile	Leu
	Thr	Ile	Leu	Gly
	Ile	Leu	Gly	Arg
	Ile	Leu	Arg	Trp
	Ile	Leu	Arg	Cys
	Ile	Leu	Arg	Gly
	Ile	Leu	Arg	Ser
	Ile	Leu	Arg	Gly
129		115	120	125
131	Val	Pro	Gly	Lys
	Pro	Gly	Lys	Gln
	Gly	Lys	Gln	Ile
	Lys	Gln	Ile	Arg
	Gly	Gln	Ile	Arg
	Gly	Gln	Ile	Phe
	Gly	Gln	Ile	Gly
	Gly	Gln	Ile	Arg
132		130	135	140
134	Val	Ser	Asp	Glu
	Ser	Asp	Glu	Tyr
	Asp	Glu	Tyr	Phe
	Glu	Tyr	Phe	Pro
	Tyr	Phe	Pro	Gly
	Phe	Pro	Gly	Phe
	Pro	Gly	Phe	Cys
	Gly	Phe	Cys	Ile
	Phe	Cys	Ile	His
	Cys	Ile	His	Tyr
135	145	150	155	160
137	Asn	Ile	Val	Met
	Ile	Val	Met	Pro
	Val	Met	Pro	Gln
	Met	Pro	Gln	Phe
	Pro	Gln	Phe	Thr
	Gln	Phe	Thr	Glu
	Phe	Thr	Glu	Ala
	Thr	Glu	Ala	Val
	Glu	Ala	Val	Ser
	Ala	Val	Ser	Pro
	Val	Ser	Pro	Val
	Ser	Pro	Val	Leu
138		165	170	175

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140 Pro Pro Ser Ala Leu Pro Leu Asp Leu Leu Asn Asn Ala Ile Thr Ala  
 141 180 185 190  
 143 Phe Ser Thr Leu Glu Asp Leu Ile Arg Tyr Leu Glu Pro Glu Arg Trp  
 144 195 200 205  
 146 Gln Leu Asp Leu Glu Asp Leu Tyr Arg Pro Thr Trp Gln Leu Leu Gly  
 147 210 215 220  
 149 Lys Ala Phe Val Phe Gly Arg Lys Ser Arg Val Val Asp Leu Asn Leu  
 150 225 230 235 240  
 152 Leu Thr Glu Glu Val Arg Leu Tyr Ser Cys Thr Pro Arg Asn Phe Ser  
 153 245 250 255  
 155 Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp Thr Ile Phe Trp Pro  
 156 260 265 270  
 158 Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala Cys Cys Leu  
 159 275 280 285  
 161 His Asn Cys Asn Glu Cys Gln Cys Val Pro Ser Lys Val Thr Lys Lys  
 162 290 295 300  
 164 Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr Gly Val Arg Gly Leu  
 165 305 310 315 320  
 167 His Lys Ser Leu Thr Asp Val Ala Leu Glu His His Glu Glu Cys Asp  
 168 325 330 335  
 170 Cys Val Cys Arg Gly Ser Thr Gly Gly  
 171 340 345  
 174 <210> SEQ ID NO: 3  
 175 <211> LENGTH: 1035  
 176 <212> TYPE: DNA  
 177 <213> ORGANISM: Homo sapiens  
 179 <400> SEQUENCE: 3  
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 181 caggcgaaat ccaacctgag tagtaaatttc cagttttcca gcaacaagga acagaacgga 120  
 182 gtacaagatc ctcatcgatgaa gagaattttt actgtgtcta ctaatggaaat tattcacagc 180  
 183 ccaagggttc ctcatctta tccaaagaaat acggctttgg tatggagatt agtagcgtt 240  
 184 gaggaaaatg tatgataca acttacgtt gatgaaaat ttggcgttgc agacccagaa 300  
 185 gatgacatat gcaagtatga ttttgtagaa gttgaggaac ccagtatgg aactatatta 360  
 186 gggcgcttgtt gtgggtctgg tactgtacca ggaaaacaga tttctaaagg aaatcaaatt 420  
 187 aggataagat ttgtatctga tgaatatttt ccttctgaac caggggtctg catccactac 480  
 188 aacattgtca tgccacaatt cacagaagct gtgagtcctt cagtgcatacc cccttcagct 540  
 189 ttgccactgg acctgtttaa taatgtata actgcctta gtaccttgg agaccttatt 600  
 190 cgatatctg aaccagagag atggcgtt gacttagaaat atcttatata gccaacttgg 660  
 191 caacttctg gcaaggcttt tgtttttggaa agaaaatcca gagtggttggaa tctgaacctt 720  
 192 ctaacagagg aggttaagatt atacagctgc acacccgttta acttctcgtt gtccataagg 780  
 193 gaagaactaa agagaaccgaa taccattttcc tggccaggtt gtctccgtt taaaacgtgt 840  
 194 ggtggaaact gtgcgttgc tctccacaat tgcaatgaat gtcaatgtgt cccaaagcaaa 900  
 195 gttactaaaa aataccacgaa ggtccttcag ttgagaccaa agaccgggtt caggggattt 960  
 196 cacaaatcac tcaccgacgt ggccctggag caccatgagg agtgtgactt tttgtgcaga 1020  
 197 gggagcacag gagga 1035  
 199 <210> SEQ ID NO: 4  
 200 <211> LENGTH: 22  
 201 <212> TYPE: DNA  
 202 <213> ORGANISM: Artificial Sequence

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204 <220> FEATURE:  
205 <223> OTHER INFORMATION: Description of Artificial Sequence: primer  
207 <400> SEQUENCE: 4  
208 aaaatgtatg gatacaaactt ac 22  
210 <210> SEQ ID NO: 5  
211 <211> LENGTH: 23  
212 <212> TYPE: DNA  
213 <213> ORGANISM: Artificial Sequence  
215 <220> FEATURE:  
216 <223> OTHER INFORMATION: Description of Artificial Sequence: primer  
218 <400> SEQUENCE: 5  
219 gtttgatgaa agatttggc ttg 23  
221 <210> SEQ ID NO: 6  
222 <211> LENGTH: 22  
223 <212> TYPE: DNA  
224 <213> ORGANISM: Artificial Sequence  
226 <220> FEATURE:  
227 <223> OTHER INFORMATION: Description of Artificial Sequence: primer  
229 <400> SEQUENCE: 6  
230 tttctaaagg aaatcaaatt ag 22  
232 <210> SEQ ID NO: 7  
233 <211> LENGTH: 20  
234 <212> TYPE: DNA  
235 <213> ORGANISM: Artificial Sequence  
237 <220> FEATURE:  
238 <223> OTHER INFORMATION: Description of Artificial Sequence: primer  
240 <400> SEQUENCE: 7  
241 gataagatt gtatctgatg 20  
243 <210> SEQ ID NO: 8  
244 <211> LENGTH: 17  
245 <212> TYPE: DNA  
246 <213> ORGANISM: Artificial Sequence  
248 <220> FEATURE:  
249 <223> OTHER INFORMATION: Description of Artificial Sequence: primer  
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252 gatgtctcct ctttcag 17  
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255 <211> LENGTH: 18  
256 <212> TYPE: DNA  
257 <213> ORGANISM: Artificial Sequence  
259 <220> FEATURE:  
260 <223> OTHER INFORMATION: Description of Artificial Sequence: primer  
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266 <211> LENGTH: 18  
267 <212> TYPE: DNA  
268 <213> ORGANISM: Artificial Sequence  
270 <220> FEATURE:

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271 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
273 <400> SEQUENCE: 10
274 agcacctgat tccgttgc 18
276 <210> SEQ ID NO: 11
277 <211> LENGTH: 20
278 <212> TYPE: DNA
279 <213> ORGANISM: Artificial Sequence
281 <220> FEATURE:
282 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
284 <400> SEQUENCE: 11
285 tagtacatag aatgttctgg 20
287 <210> SEQ ID NO: 12
288 <211> LENGTH: 19
289 <212> TYPE: DNA
290 <213> ORGANISM: Artificial Sequence
292 <220> FEATURE:
293 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
295 <400> SEQUENCE: 12
296 aagagacata cttctgtac 19
298 <210> SEQ ID NO: 13
299 <211> LENGTH: 21
300 <212> TYPE: DNA
301 <213> ORGANISM: Artificial Sequence
303 <220> FEATURE:
304 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
306 <400> SEQUENCE: 13
307 ccaggtacaa taagtgaact g 21
309 <210> SEQ ID NO: 14
310 <211> LENGTH: 28
311 <212> TYPE: DNA
312 <213> ORGANISM: Artificial Sequence
314 <220> FEATURE:
315 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
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321 <211> LENGTH: 31
322 <212> TYPE: DNA
323 <213> ORGANISM: Artificial Sequence
325 <220> FEATURE:
326 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
328 <400> SEQUENCE: 15
329 gaaaaatatt catcagatac aaatcttatac c 31
331 <210> SEQ ID NO: 16
332 <211> LENGTH: 22
333 <212> TYPE: DNA
334 <213> ORGANISM: Artificial Sequence
336 <220> FEATURE:
337 <223> OTHER INFORMATION: Description of Artificial Sequence: primer

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→ Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY  
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Input Set : A:\seqlistJAB1463corrected.app.txt  
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L:568 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:30  
L:572 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:30  
L:577 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30  
L:581 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30  
L:622 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:33  
L:630 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33  
L:701 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:38  
L:705 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:38  
L:709 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:38  
L:713 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38  
L:715 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38  
L:743 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:40  
L:747 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:40  
L:751 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:40  
L:756 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40  
L:757 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40  
L:759 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40  
L:800 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:43  
L:804 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:43  
L:808 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:43  
L:812 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:43  
L:819 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43  
L:820 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43  
L:831 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:44  
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L:839 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:44  
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L:847 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:44  
L:851 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:44  
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L:859 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:44  
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L:867 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:44  
L:873 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44  
L:874 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44  
L:875 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44  
L:876 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44  
L:887 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:45  
L:891 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:45  
L:895 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:45  
L:903 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45  
L:904 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45  
L:929 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:47  
L:933 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47  
L:962 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:49  
L:966 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:49  
L:971 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49  
L:975 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49

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L:1001 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:51  
L:1005 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:51  
L:1009 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51  
L:1013 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51  
L:1055 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:54  
L:1063 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54  
L:1164 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:61  
L:1168 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:61  
L:1172 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:61  
L:1177 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61  
L:1179 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61  
L:1192 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:62  
L:1196 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:62  
L:1200 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62  
L:1204 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62  
L:1215 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:63  
L:1223 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63  
L:1279 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:67  
L:1283 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:67  
L:1289 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:67  
L:1291 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:67  
L:1303 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:68  
L:1307 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:68  
L:1311 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:68  
L:1315 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:68  
L:1316 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:68  
L:1318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:68  
L:1373 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:72  
L:1377 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72  
L:1391 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:73  
L:1395 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:73  
L:1425 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:75  
L:1429 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:75  
L:1433 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:75  
L:1437 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:75  
L:1445 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75  
L:1446 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75  
L:1457 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:76  
L:1468 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76  
L:1523 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:77  
L:1524 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:77  
L:1525 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:77  
L:1526 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:77  
L:1547 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:78  
L:1548 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:78  
L:1569 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:79  
L:1601 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:80  
L:1602 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:80  
L:1605 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:80

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/869,198A

DATE: 02/13/2002

TIME: 18:51:02

Input Set : A:\seqlistJAB1463corrected.app.txt  
Output Set: N:\CRF3\02132002\I869198A.raw

L:1622 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:81

L:1623 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:81

L:1665 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:83